

SEQUENCE LISTING

<110> SHITARA, KENYA
 HOSAKA, EMI
 NATSUME, AKITO
 WAKITANI, MASAKO
 UCHIDA, KAZUHISA
 SATOH, MITSUO
 OHNUKI, NAKOO
 NAKAMAURA, KAZUYASU

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<130> BJS-249-426

<140> 10/575,261
 <141> 2006-04-10

<150> PCT/JP04/15325
 <151> 2004-10-08

<150> JP 2003-350158
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ggc cag gat ggc tca tac ttg gca gaa ttc ctg ctg gag aaa gga tac 144
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Lys Leu His Tyr Gly Asp Leu Thr Asp Ser Thr Cys Leu Val Lys Ile	
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His Val Lys Ile Ser Phe Asp Leu Ala Glu Tyr Thr Ala Asp Val Asp	
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Gly Val Gly Thr Leu Arg Leu Leu Asp Ala Ile Lys Thr Cys Gly Leu	
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 325 330 335

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Glu Val His Gly Ile Val Arg Arg Ser Ser Ser Phe Asn Thr Gly Arg
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Lys Leu His Tyr Gly Asp Leu Thr Asp Ser Thr Cys Leu Val Lys Ile
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Ile Asn Glu Val Lys Pro Thr Glu Ile Tyr Asn Leu Gly Ala Gln Ser
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His Val Lys Ile Ser Phe Asp Leu Ala Glu Tyr Thr Ala Asp Val Asp
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145 150 155 160

Lys Val Gln Glu Ile Pro Gln Lys Glu Thr Thr Pro Phe Tyr Pro Arg
165 170 175

Ser Pro Tyr Gly Ala Ala Lys Leu Tyr Ala Tyr Trp Ile Val Val Asn
180 185 190

Phe Arg Glu Ala Tyr Asn Leu Phe Ala Val Asn Gly Ile Leu Phe Asn
195 200 205

His Glu Ser Pro Arg Arg Gly Ala Asn Phe Val Thr Arg Lys Ile Ser
210 215 220

Arg Ser Val Ala Lys Ile Tyr Leu Gly Gln Leu Glu Cys Phe Ser Leu
225 230 235 240

Gly Asn Leu Asp Ala Lys Arg Asp Trp Gly His Ala Lys Asp Tyr Val
245 250 255

Glu Ala Met Trp Leu Met Leu Gln Asn Asp Glu Pro Glu Asp Phe Val
260 265 270

Ile Ala Thr Gly Glu Val His Ser Val Arg Glu Phe Val Glu Lys Ser
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Phe Met His Ile Gly Lys Thr Ile Val Trp Glu Gly Lys Asn Glu Asn
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Glu Val Gly Arg Cys Lys Glu Thr Gly Lys Ile His Val Thr Val Asp
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Leu Lys Tyr Tyr Arg Pro Thr Glu Val Asp Phe Leu Gln Gly Asp Cys
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Ser Lys Ala Gln Gln Lys Leu Asn Trp Lys Pro Arg Val Ala Phe Asp
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Thr Asp Ala Ala Gln Thr Gln Ala Leu Phe Gln Lys Val Gln Pro Thr
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His Val Ile His Leu Ala Ala Met Val Gly Gly Leu Phe Arg Asn Ile
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Lys Tyr Asn Leu Asp Phe Trp Arg Lys Asn Val His Ile Asn Asp Asn
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Val Leu His Ser Ala Phe Glu Val Gly Thr Arg Lys Val Val Ser Cys
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Leu Ser Thr Cys Ile Phe Pro Asp Lys Thr Thr Tyr Pro Ile Asp Glu
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Thr Met Ile His Asn Gly Pro Pro His Ser Ser Asn Phe Gly Tyr Ser
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His Gly Cys Thr Phe Thr Ala Val Ile Pro Thr Asn Val Phe Gly Pro
165 170 175

His Asp Asn Phe Asn Ile Glu Asp Gly His Val Leu Pro Gly Leu Ile
180 185 190

His Lys Val His Leu Ala Lys Ser Asn Gly Ser Ala Leu Thr Val Trp
195 200 205

Gly Thr Gly Lys Pro Arg Arg Gln Phe Ile Tyr Ser Leu Asp Leu Ala
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Arg Leu Phe Ile Trp Val Leu Arg Glu Tyr Asn Glu Val Glu Pro Ile
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Ile Leu Ser Val Gly Glu Glu Asp Glu Val Ser Ile Lys Glu Ala Ala
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Glu Ala Val Val Glu Ala Met Asp Phe Cys Gly Glu Val Thr Phe Asp
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Ser Thr Lys Ser Asp Gly Gln Tyr Lys Lys Thr Ala Ser Asn Gly Lys
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Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr
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Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
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Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val
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Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
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Arg Pro Gln Pro Trp Leu Glu Arg Glu Ile Glu Glu Thr Thr Lys Lys
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Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
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Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
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Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
 435 440 445

Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
 450 455 460

Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
 465 470 475 480

Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
 485 490 495

Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro
500 505 510

His Lys Pro Arg Thr Glu Glu Glu Ile Pro Met Glu Pro Gly Asp Ile
515 520 525

Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Ile Asn
530 535 540

Arg Lys Leu Gly Lys Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
545 550 555 560

Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys
565 570 575

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<210> 9
<211> 5
<212> PRT
<213> Mus musculus
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<400> 9
Asp His Ala Ile His
1             5
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<210> 10
<211> 17
<212> PRT
<213> Mus musculus
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<400> 10
Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe Lys
1          5          10          15
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Gly

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<210> 11
<211> 6
<212> PRT
<213> Mus musculus
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<400> 11
Ser Leu Asn Met Ala Tyr
1           5
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<210> 12
 <211> 17
 <212> PRT
 <213> Mus musculus

<400> 12
 Lys Ser Ser Gln Ser Leu Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu
 1 5 10 15

Ala

<210> 13
 <211> 7
 <212> PRT
 <213> Mus musculus

<400> 13
 Trp Ala Ser Ala Arg Glu Ser
 1 5

<210> 14
 <211> 9
 <212> PRT
 <213> Mus musculus

<400> 14
 Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr
 1 5

<210> 15
 <211> 115
 <212> PRT
 <213> Mus musculus

<400> 15
 Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Val Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
100 105 110

Val Ser Ser
115

<210> 16

<211> 113

<212> PRT

<213> Mus musculus

<400> 16

Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Pro Val Ser Val Gly
1 5 10 15

Glu Lys Val Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ala Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser
65 70 75 80

Ile Ser Ser Val Lys Thr Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Val Leu
100 105 110

Lys

<210> 17

<211> 265

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic protein

<400> 17

Met	Glu	Trp	Ser	Trp	Val	Phe	Leu	Phe	Phe	Leu	Ser	Val	Thr	Thr	Gly
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Val	His	Ser	Gln	Val	Gln	Leu	Gln	Gln	Ser	Asp	Ala	Glu	Leu	Val	Lys
			20				25						30		
Pro	Gly	Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
		35					40					45			
Thr	Asp	His	Ala	Ile	His	Trp	Val	Lys	Gln	Asn	Pro	Glu	Gln	Gly	Leu
	50					55					60				
Glu	Trp	Ile	Gly	Tyr	Phe	Ser	Pro	Gly	Asn	Asp	Asp	Phe	Lys	Tyr	Asn
65					70					75					80
Glu	Arg	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser
			85						90					95	
Thr	Ala	Tyr	Val	Gln	Leu	Asn	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val
			100					105					110		
Tyr	Phe	Cys	Thr	Arg	Ser	Leu	Asn	Met	Ala	Tyr	Trp	Gly	Gln	Gly	Thr
		115				120						125			
Ser	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
	130					135					140				
Gly	Gly	Gly	Gly	Ser	Asp	Ile	Val	Met	Ser	Gln	Ser	Pro	Ser	Ser	Leu
145					150					155					160
Pro	Val	Ser	Val	Gly	Glu	Lys	Val	Thr	Leu	Ser	Cys	Lys	Ser	Ser	Gln
				165				170						175	
Ser	Leu	Leu	Tyr	Ser	Gly	Asn	Gln	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln
			180					185					190		
Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Ala
		195					200					205			
Arg	Glu	Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr
	210					215					220				

Asp Phe Thr Leu Ser Ile Ser Ser Val Lys Thr Glu Asp Leu Ala Val
 225 230 235 240

Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly
 245 250 255

Thr Lys Leu Val Leu Lys Arg Ala Ala
 260 265

<210> 18

<211> 463

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 18

ccggaattcg acccctcacc atggaatgga gctgggtctt tctcttcttc ctgtcagtaa	60
ctacaggtgt ccaactccag gttcagttgc agcagtctga cgctgagttg gtgaaacctg	120
gggcttcagt gaagatttcc tgcaaggctt ctggctacac ctctactgac catgcaattc	180
actgggtgaa acagaaccct gaacagggcc tggaatggat tggatatctt tctcccgaa	240
atgatgattt taaatacaat gagagggtca agggcaaggc cacactgact gcagacaaat	300
cctccagcac tgcctacgtg cagctcaaca gcctgacatc tgaggattct gcagtgtatt	360
tctgtaccag atccctgaat atggcctact ggggtcaagg aacctcagtc accgtctcct	420
caggtggcgg aggcagcgga ggcggtggct ccggaactag tcc	463

<210> 19

<211> 129

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 19

ccggaattcg acccctcacc atggaatgga gctgggtctt tctcttcttc ctgtcagtaa	60
ctacaggtgt ccaactccag gttcagttgc agcagtctga cgctgagttg gtgaaacctg	120
gggcttcag	129

<210> 20
 <211> 134
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 20
 catttccggg agaaaaatat ccaatccatt ccaggccctg ttcagggttc tgtttcacc 60
 agtgaattgc atggtcagtg aagggtgtagc cagaagcctt gcaggaaatc ttcactgaag 120
 ccccagggtt cacc 134

<210> 21
 <211> 131
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 21
 ggatattttt ctcccggaaa tgatgatttt aaatacaatg agagggttcaa gggcaaggcc 60
 aactgactg cagacaaatc ctccagcact gcctacgtgc agctcaacag cctgacatct 120
 gaggattctg c 131

<210> 22
 <211> 132
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 22
 ggactagtgc cggagccacc gcctccgctg cctccgccac ctgaggagac ggtgactgag 60
 gttccttgac cccagtaggc catattcagg gatctggtac agaaatacac tgcagaatcc 120
 tcagatgtca gg 132

<210> 23
 <211> 536
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 23

cgggaattct cggaggcgg aggctcggac attgtgatgt cacagtctcc atcctcccta	60
cctgtgtcag ttggcgagaa ggttactttg agctgcaagt ccagtcagag ccttttatat	120
agtggtaatc aaaagaacta ctggcctgg taccagcaga aaccagggca gtctcctaaa	180
ctgctgattt actgggcacg cgctagggaa tctggggctc ctgctcgctt cacaggcagt	240
ggatctggga cagatttcac tctctccatc agcagtgtga agactgaaga cctggcagtt	300
tattactgtc agcagtatta tagctatccc ctacggttcg gtgctgggac caagctggtg	360
ctgaacggg cgcgcgagcc caaatctctt gacaaaactc acacgtgccc accgtgccca	420
gcacctgaac tcttgggggg accgtcagtc ttcctcttcc ccccaaaacc caaggacacc	480
ctcatgatct cccggacccc tgagggtcac tgcgtggtgg tggacgtgac tagtcc	536

<210> 24

<211> 150

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 24

tctgaattct cggaggcgg aggctcggac attgtgatgt cacagtctcc atcctcccta	60
cctgtgtcag ttggcgagaa ggttactttg agctgcaagt ccagtcagag ccttttatat	120
agtggtaatc aaaagaacta ctggcctgg	150

<210> 25

<211> 150

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 25

cacactgctg atggagagag tgaaatctgt ccagatcca ctgcctgtga agcgatcagg	60
gacccagat tccctagcgg atgccagta aatcagcagt ttaggagact gccctggttt	120
ctgctggtac caggccaagt agttctttttg	150

<210> 26
 <211> 149
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 26
 ctctctccat cagcagtggt aagactgaag acctggcagt ttattactgt cagcagtatt 60
 atagctatcc cctcacgttc ggtgctggga ccaagctggt gctgaaacgg gccgccgagc 120
 ccaaatctcc tgacaaaact cacacgtgc 149

<210> 27
 <211> 149
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 27
 ggactagtcg cgtccaccac cagcagtggt acctcagggg tccgggagat catgaggggtg 60
 tccttgggtt ttggggggaa gaggaagact gacggtcccc ccaggagttc aggtgctggg 120
 cacggtgggc acgtgtgagt ttgtcagg 149

<210> 28
 <211> 526
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 28
 caggaaacag ctatgacggt accgaattcg cgaggcaggc agcctggaga gaaggcgctg 60
 ggctgcgagg gcgcgagggc gcgagggcag ggggcaaccg gacccccccc gcatccatgg 120
 cgcccctcgc cgtctgggccc gcgctggccg tcggactgga gctctgggct gcggcgcacg 180
 ccttgccccc ccagggtggca ttacacct acgccccgga gccccgggagc acatgcgggc 240
 tcagagaata ctatgaccag acagctcaga tgtgtcgag caaatgctcg ccgggccaac 300
 atgcaaaagt cttctgtacc aagacctcgg acaccgtgtg tgactcctgt gagggacagca 360
 cataccacca gctctggaac tgggttcccc agtgcttgag ctgtggctcc cgctgtagct 420

ctgaccaggt ggaaactcaa gcctgcactc gggaacagaa ccgcattctgc acctgcaggc 480
 ccggctggta ctgcgcgtcg agcaagctta ctggccgtcg ttttac 526

<210> 29
 <211> 537
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 29
 caggaaacag ctatgacggt accgctgagc aagcaggagg ggtgccggct gtgcgcgcog 60
 ctgcgcaagt gccgcccggg cttcggcgctg gccagaccag gaactgaaac atcagacgtg 120
 gtgtgcaagc cctgtgcccc ggggacgttc tccaacacga cttcatccac ggatatttgc 180
 aggccccacc agatctgtaa cgtggtggcc atccctggga atgcaagcat ggatgcagtc 240
 tgcacgtcca cgtccccac ccggagtatg gccccagggg cagtacactt accccagcca 300
 gtgtccacac gatcccaaca cagcagcca actccagaac ccagcactgc tccaagcacc 360
 tccttctctg tcccaatggg cccagcccc ccagctgaag ggagcactgg cgacgagccc 420
 aaatcttgtg acaaaactca cacatgccca ccgtgccag cacctgaact cctgggggga 480
 ccgtcagctc tcctcttccc cccaaaaccc aaggaagctt actggccgtc gttttac 537

<210> 30
 <211> 150
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 30
 atggcgcccc tcgccgtctg ggccgcgctg gccgtcggac tggagctctg ggctgcggcg 60
 cagccttctg ccgcccagggt ggcatattaca ccttacgccc cggagccccg gagcacatgc 120
 cggctcagag aatactatga ccagacagct 150

<210> 31
 <211> 135
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 31
 agacggcgac gggcgccatg gatgcgggcg gggtcgggtt gccccctgcc ctgcgcacct 60
 cgcgcctcgc cagccacgag ccttctctcc aggctgcctg cctcggaat tcggtaccgt 120
 catagctgtt tcctg 135

<210> 32
 <211> 150
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 32
 gaactgggtt cccgagtgtc tgaactgtgg ctcccgtgt agctctgacc aggtggaaac 60
 tcaagcctgc actcgggaac agaaccgcat ctgcacctgc aggcccggtt ggtactgcgc 120
 gctgagcaag cttactggcc gtcgttttac 150

<210> 33
 <211> 150
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 33
 gcaactcggga acccagttcc agagctgggt gtatgtgctg tcttcacagg agtcacacac 60
 ggtgtccgag gtcttggtag agaagacttt tgcattgttg cccggcgagc atttgcgtga 120
 gcacatctga gctgtctggt catagtattc 150

<210> 34
 <211> 149
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 34
 ctgtgccccg gggacgttct ccaacacgac ttcattccag gatatttgca ggccccacca 60

gatctgtaac gtggtggcca tccctgggaa tgcaagcatg gatgcagtct gcacgtccac 120
gtccccacc cggagtatgg ccccgagg 149

<210> 35
<211> 150
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 35
gaacgtcccc ggggcacagg gcttgacac cacgtctgat gtttcagttc ctggtctggc 60
cacgccgaag cccggggcgg acttgccgag cggcgcgcac agccggcacc cctcctgctt 120
gctcagcggg accgtcatag ctgtttcctg 150

<210> 36
<211> 145
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 36
agctgaagg agcactggcg acgagccaa atcttgtgac aaaactcaca catgccacc 60
gtgccagca cctgaactcc tggggggacc gtcagtcttc ctcttcccc caaaacccaa 120
ggaagcttac tggccgtcgt ttac 145

<210> 37
<211> 150
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 37
gccagtgtcc ccttcagctg gggggctggg gccattggg agcaggaagg aggtgcttgg 60
agcagtgtc gggtctggag ttggctgcgt gtgttgggat cgtgtggaca ctggctgggg 120
taagtgtact gcccctgggg ccatactccg 150

<210> 38
 <211> 452
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 38
 caggaaacag ctatgacggt accgaattcc gacgagccat gggtgtctggg agcgacgcgg 60
 ggcgggccct ggggggtctc agcgtggtct gcctgctgca ctgctttggt ttcatacagct 120
 gtttttccca acaaatatat ggtgtgtgtg atgggaatgt aactttccat gtaccaagca 180
 atgtgccttt aaaagaggtc ctatggaaaa aacaaaagga taaagttgca gaactggaaa 240
 attctgaatt cagagctttc tcattcttta aaaatagggt ttatttagac actgtgtcag 300
 gtacgctcac tatctacaac ttaacatcat cagatgaaga tgagatgaa atggaatgcg 360
 caaatattac tgataccatg aagtcttttc ttatgtcga caaaactcac acatgcccac 420
 cgtgcccagc acctgactgg ccgtcgtttt ac 452

<210> 39
 <211> 138
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 39
 gtttcacag ctgtttttcc caacaaatat atgggtgtgt gtaggggaat gtaactttcc 60
 atgtaccaag caatgtgcct ttaaaagagg tcctatggaa aaaacaaaag gataaagttg 120
 cagaactgga aaattctg 138

<210> 40
 <211> 129
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 40
 gggaaaaaca gctgatgaaa ccaaagcagt gcagcaggca gaccacgctg aggaccccca 60
 gggcccgccc cgcgtcgctc ccagcaacca tggctcgctg gaattcggtg ccgtcatagc 120

tgtttcctg

129

<210> 41

<211> 133

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 41

cttaacatca tcagatgaag atgagtatga aatggaatcg ccaaatatta ctgataccat 60

gaagttcttt ctttatgtcg acaaaactca cacatgccca ccggtgccag cacctgactg 120

gccgtcggtt tac 133

<210> 42

<211> 118

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 42

catcttcato tgaatgatgtt aagttgtaga tagtgaggct acctgacaca gtgtctaaat 60

aaaccttatt tttaaaagat gagaaagctc tgaattcaga attttccagt tctgcaac 118

<210> 43

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 43

gtaaaacgac ggccagt 17

<210> 44

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 44
 taaatagaat tcggcatcat gtggcagctg ct 32

<210> 45
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 45
 aataaaggat cctgggggtca ttgtcttga ggggt 34

<210> 46
 <211> 788
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (13)..(774)

<400> 46
 gaattcggca tc atg tgg cag ctg ctc ctc cca act gct ctg cta ctt cta 51
 1 5 10
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gtt tca gct ggc atg cgg act gaa gat ctc cca aag gct gtg gtg ttc 99
 Val Ser Ala Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe
 15 20 25

ctg gag cct caa tgg tac agg gtg ctc gag aag gac agt gtg act ctg 147
 Leu Glu Pro Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu
 30 35 40 45

aag tgc cag gga gcc tac tcc cct gag gac aat tcc aca cag tgg ttt 195
 Lys Cys Gln Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe
 50 55 60

cac aat gag agc ctc atc tca agc cag gcc tcg agc tac ttc att gac 243
 His Asn Glu Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp
 65 70 75

gct gcc aca gtc gac gac agt gga gag tac agg tgc cag aca aac ctc 291
 Ala Ala Thr Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu
 80 85 90

tcc acc ctc agt gac cgg gtg cag cta gaa gtc cat atc ggc tgg ctg 339
 Ser Thr Leu Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu
 95 100 105

ttg ctc cag gcc cct cgg tgg gtg ttc aag gag gaa gac cct att cac 387
 Leu Leu Gln Ala Pro Arg Trp Val Phe Lys Glu Asp Pro Ile His
 110 115 120 125

 ctg agg tgt cac agc tgg aag aac act gct ctg cat aag gtc aca tat 435
 Leu Arg Cys His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr
 130 135 140

 tta cag aat ggc aaa ggc agg aag tat ttt cat cat aat tct gac ttc 483
 Leu Gln Asn Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe
 145 150 155

 tac att cca aaa gcc aca ctc aaa gac agc ggc tcc tac ttc tgc agg 531
 Tyr Ile Pro Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg
 160 165 170

 ggg ctt ttt ggg agt aaa aat gtg tct tca gag act gtg aac atc acc 579
 Gly Leu Phe Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr
 175 180 185

 atc act caa ggt ttg gca gtg tca acc atc tca tca ttc ttt cca cct 627
 Ile Thr Gln Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro
 190 195 200 205

 ggg tac caa gtc tct ttc tgc ttg gtg atg gta ctc ctt ttt gca gtg 675
 Gly Tyr Gln Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val
 210 215 220

 gac aca gga cta tat ttc tct gtg aag aca aac att cga agc tca aca 723
 Asp Thr Gly Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr
 225 230 235

 aga gac tgg aag gac cat aaa ttt aaa tgg aga aag gac cct caa gac 771
 Arg Asp Trp Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp
 240 245 250

 aaa tgacccagg atcc 788
 Lys

<210> 47
 <211> 254
 <212> PRT
 <213> Homo sapiens

<400> 47
 Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Val Ser Ala
 1 5 10 15

Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
 20 25 30

Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
 35 40 45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
50 55 60

Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
65 70 75 80

Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
85 90 95

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
100 105 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
115 120 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
130 135 140

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
145 150 155 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Phe
165 170 175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
180 185 190

Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln
195 200 205

Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
210 215 220

Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg Asp Trp
225 230 235 240

Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys
245 250

<210> 48

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ctg gag cct caa tgg tac agg gtg ctc gag aag gac agt gtg act ctg	147
Leu Glu Pro Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu	
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aag tgc cag gga gcc tac tcc cct gag gac aat tcc aca cag tgg ttt	195
Lys Cys Gln Gly Ala Tyr Ser Pro Glu Asn Ser Thr Gln Trp Phe	
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cac aat gag agc ctc atc tca agc cag gcc tcg agc tac ttc att gac	243
His Asn Glu Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp	
65 70 75	
gct gcc aca gtc gac gac agt gga gag tac agg tgc cag aca aac ctc	291
Ala Ala Thr Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu	
80 85 90	
tcc acc ctc agt gac ccg gtg cag cta gaa gtc cat atc ggc tgg ctg	339
Ser Thr Leu Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu	
95 100 105	
ttg ctc cag gcc cct cgg tgg gtg ttc aag gag gaa gac cct att cac	387
Leu Leu Gln Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His	
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ctg agg tgt cac agc tgg aag aac act gct ctg cat aag gtc aca tat	435
Leu Arg Cys His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr	
130 135 140	
tta cag aat ggc aaa ggc agg aag tat ttt cat cat aat tct gac ttc	483
Leu Gln Asn Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe	
145 150 155	
tac att cca aaa gcc aca ctc aaa gac agc ggc tcc tac ttc tgc agg	531
Tyr Ile Pro Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg	
160 165 170	
ggg ctt gtt ggg agt aaa aat gtg tct tca gag act gtg aac atc acc	579
Gly Leu Val Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr	
175 180 185	
atc act caa ggt ttg gca gtg tca acc atc tca tca ttc ttt cca cct	627
Ile Thr Gln Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro	
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723

771

788

<213> Homo sapiens

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Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val
 165 170 175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
 180 185 190

Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln
 195 200 205

Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
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<213> Artificial Sequence

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<211> 620

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<220>

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<222> (13)..(609)

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51

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 Leu Glu Pro Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu
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 Lys Cys Gln Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe
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cac aat gag agc ctc atc tca agc cag gcc tcg agc tac ttc att gac 243
 His Asn Glu Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp
 65 70 75

gct gcc aca gtc gac gac agt gga gag tac agg tgc cag aca aac ctc 291
 Ala Ala Thr Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu
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tcc acc ctc agt gac ccg gtg cag cta gaa gtc cat atc ggc tgg ctg 339
 Ser Thr Leu Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu
 95 100 105

ttg ctc cag gcc cct cgg tgg gtg ttc aag gag gaa gac cct att cac 387
 Leu Leu Gln Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His
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ctg agg tgt cac agc tgg aag aac act gct ctg cat aag gtc aca tat 435
 Leu Arg Cys His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr
 130 135 140

tta cag aat ggc aaa ggc agg aag tat ttt cat cat aat tct gac ttc 483
 Leu Gln Asn Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe
 145 150 155

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 Tyr Ile Pro Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg
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 Gly Leu Phe Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr
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 35 40 45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
 50 55 60

Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
 65 70 75 80

Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
 85 90 95

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
 100 105 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
 115 120 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
 130 135 140

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
 145 150 155 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Phe
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Gly His His His His His His
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Val Ser Ala Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe
15 20 25

ctg gag cct caa tgg tac agg gtg ctc gag aag gac agt gtg act ctg 147
Leu Glu Pro Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu
30 35 40 45

aag tgc cag gga gcc tac tcc cct gag gac aat tcc aca cag tgg ttt 195
Lys Cys Gln Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe
50 55 60

cac aat gag agc ctc atc tca agc cag gcc tcg agc tac ttc att gac 243
His Asn Glu Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp
65 70 75

gct gcc aca gtc gac gac agt gga gag tac agg tgc cag aca aac ctc 291
Ala Ala Thr Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu
80 85 90

tcc acc ctc agt gac ccg gtg cag cta gaa gtc cat atc ggc tgg ctg 339
Ser Thr Leu Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu
95 100 105

ttg ctc cag gcc cct cgg tgg gtg ttc aag gag gaa gac cct att cac 387
Leu Leu Gln Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His
110 115 120 125

ctg agg tgt cac agc tgg aag aac act gct ctg cat aag gtc aca tat 435
Leu Arg Cys His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr
130 135 140

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Leu Gln Asn Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe
145 150 155

tac att cca aaa gcc aca ctc aaa gac agc ggc tcc tac ttc tgc agg 531
Tyr Ile Pro Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg
160 165 170

ggg ctt gtt ggg agt aaa aat gtg tct tca gag act gtg aac atc acc 579
Gly Leu Val Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr
175 180 185

atc act caa ggt cat cat cat cat cat cat tgacaggatc c 620
Ile Thr Gln Gly His His His His His His
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 20 25 30

Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
 35 40 45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
 50 55 60

Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
 65 70 75 80

Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
 85 90 95

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
 100 105 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
 115 120 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
 130 135 140

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
 145 150 155 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val
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Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
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<210> 56
<211> 28
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

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<400> 56
gagacttcag cccacttcaa ttattggc 28

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```

<210> 57
<211> 25
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

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<400> 57
cttgtgtgac tcttaactct cagag 25

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<210> 58
<211> 25
<212> DNA
<213> Artificial Sequence

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<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

 <400> 58
 gagggccactt gtgtagcgcc aagtg 25

 <210> 59
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

 <400> 59
 ccctcgagat aacttcgtat agc 23

 <210> 60
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

 <400> 60
 ggtaggcctc actaactg 18

 <210> 61
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

 <400> 61
 catagaaaca agtaacaaca gccag 25

 <210> 62
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

 <400> 62
 gtgagtccat ggctgtcact g 21

<210> 63
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 63
 cctgacttgg ctattctcag

20

<210> 64
 <211> 235
 <212> PRT
 <213> Homo sapiens

<400> 64
 Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
 1 5 10 15

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
 20 25 30

Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
 35 40 45

Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
 50 55 60

Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
 65 70 75 80

Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
 85 90 95

Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
 100 105 110

Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
 115 120 125

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
 130 135 140

Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
145 150 155 160

Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
165 170 175

Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
180 185 190

His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr
195 200 205

Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
210 215 220

Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp
225 230 235

<210> 65
<211> 92
<212> PRT
<213> Homo sapiens

<400> 65
Phe Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His
1 5 10 15

Val Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys
20 25 30

Asp Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser
35 40 45

Phe Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile
50 55 60

Tyr Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro
65 70 75 80

Asn Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val
85 90

<210> 66
<211> 5
<212> PRT
<213> Mus musculus

<400> 66
 Ser Tyr Gly Met Ser
 1 5

<210> 67
 <211> 17
 <212> PRT
 <213> Mus musculus

<400> 67
 Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys
 1 5 10 15

Gly

<210> 68
 <211> 11
 <212> PRT
 <213> Mus musculus

<400> 68
 Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr
 1 5 10

<210> 69
 <211> 10
 <212> PRT
 <213> Mus musculus

<400> 69
 Ser Ala Ser Ser Ser Val Ser Tyr Met His
 1 5 10

<210> 70
 <211> 7
 <212> PRT
 <213> Mus musculus

<400> 70
 Asp Thr Ser Lys Leu Ala Ser
 1 5

<210> 71
 <211> 9
 <212> PRT
 <213> Mus musculus

<400> 71
 Gln Gln Trp Ser Ser Asn Pro Pro Thr
 1 5

<210> 72
 <211> 120
 <212> PRT
 <213> Mus musculus

<400> 72
 Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Leu Val
 35 40 45

Ala Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Ala Arg Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr Trp Gly Pro
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 73
 <211> 109
 <212> PRT
 <213> Mus musculus

<400> 73
 Asp Ile Glu Leu Thr Gln Ser Pro Ser Ile Met Ser Ala Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Pro Thr
85 90 95

Phe Gly Gly Arg Thr Lys Leu Glu Leu Lys Arg Ala Ala
100 105

<210> 74

<211> 244

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein

<400> 74

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Leu Val
35 40 45

Ala Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr Trp Gly Pro
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ser
 130 135 140

Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala
 145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr
 165 170 175

Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
 180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
 195 200 205

Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
 210 215 220

Trp Ser Ser Asn Pro Pro Thr Phe Gly Gly Arg Thr Lys Leu Glu Leu
 225 230 235 240

Lys Arg Ala Ala

<210> 75

<211> 515

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic protein

<400> 75

Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Gly Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Leu Val
 35 40 45

Ala Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr Trp Gly Pro
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125
 Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ser
 130 135 140
 Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala
 145 150 155 160
 Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr
 165 170 175
 Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
 180 185 190
 Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
 195 200 205
 Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
 210 215 220
 Trp Ser Ser Asn Pro Pro Thr Phe Gly Gly Arg Thr Lys Leu Glu Leu
 225 230 235 240
 Lys Arg Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 245 250 255
 Gly Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln
 260 265 270
 Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys
 275 280 285
 Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His Ala Ile His
 290 295 300

Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile Gly Tyr Phe
 305 310 315 320

Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe Lys Gly Lys
 325 330 335

Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Val Gln Leu
 340 345 350

Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Thr Arg Ser
 355 360 365

Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
 370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
 385 390 395 400

Ile Val Met Ser Gln Ser Pro Ser Ser Leu Pro Val Ser Val Gly Glu
 405 410 415

Lys Val Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser Gly
 420 425 430

Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser
 435 440 445

Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ala Arg Glu Ser Gly Val Pro
 450 455 460

Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile
 465 470 475 480

Ser Ser Val Lys Thr Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln Tyr
 485 490 495

Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Val Leu Lys
 500 505 510

Arg Ala Ala
 515

<210> 76

<211> 515

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic protein

<400> 76

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30

Ala Ile His Trp Val Lys Gln Asn Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn Glu Arg Phe
 50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Val Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95

Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr Ser Val Thr
 100 105 110

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Pro Val Ser
 130 135 140

Val Gly Glu Lys Val Thr Leu Ser Cys Lys Ser Ser Gln Ser Leu Leu
 145 150 155 160

Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
 165 170 175

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ala Arg Glu Ser
 180 185 190

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
 195 200 205
 Leu Ser Ile Ser Ser Val Lys Thr Glu Asp Leu Ala Val Tyr Tyr Cys
 210 215 220
 Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
 225 230 235 240
 Val Leu Lys Arg Ala Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 245 250 255
 Gly Gly Gly Thr Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
 260 265 270
 Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
 275 280 285
 Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Gly
 290 295 300
 Met Ser Trp Val Arg Gln Thr Pro Asp Lys Arg Leu Glu Leu Val Ala
 305 310 315 320
 Thr Ile Asn Ser Asn Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys
 325 330 335
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
 340 345 350
 Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys Ala
 355 360 365
 Arg Asp Arg Asp Gly Tyr Asp Glu Gly Phe Asp Tyr Trp Gly Pro Gly
 370 375 380
 Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 385 390 395 400
 Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ser Ile
 405 410 415
 Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser
 420 425 430

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser
 435 440 445

Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro
 450 455 460

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 465 470 475 480

Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 485 490 495

Ser Ser Asn Pro Pro Thr Phe Gly Gly Arg Thr Lys Leu Glu Leu Lys
 500 505 510

Arg Ala Ala
 515

<210> 77
 <211> 89
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 77
 gaattcgacc cctcaccatg gaatggagct gggctctttct cttcttctctg tcagtaacta 60
 ccggtggggg tccccactag tctccgga 89

<210> 78
 <211> 83
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 78
 aattcgaccc ctcaccatgg aatggagctg ggtctttctc ttcttctctg cagtaactac 60
 ccggtgggat cccccactag cct 83

<210> 79
 <211> 83
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 79
 ccggaggact agtggggatc cccaccggta gttactgaca ggaagaagag aaagaccag 60
 ctccattcca tggtagggg tcg 83

<210> 80
 <211> 411
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 80
 gcgaccggtg tccactccca ggtccaactg caggagtcag gaggaggctt agtgcagcct 60
 ggagggtccc tgaactctc ctgtgcagcc tctggattca ctttcagtag ctatggcatg 120
 tcttgggttc gccagactcc agacaagagg ctggagttgg tcgcaaccat taatagtaat 180
 ggtggttagca cctattatcc agacagtgtg aagggccgat tcaccatctc cagagacaat 240
 gccagaaca cctgtacct gcaaatgagc agtctgaagt ctgaggacac agccatgtat 300
 tactgtgcaa gagatcgga tggttacgac gagggatttg actactgggg ccaggggacc 360
 acggtcaccg tctcctcagg tggcgagggc agcgaggcgc gtggatcccg c 411

<210> 81
 <211> 120
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 81
 gcgaccggtg tccactccca ggtccaactg caggagtcag gaggaggctt agtgcagcct 60
 ggagggtccc tgaactctc ctgtgcagcc tctggattca ctttcagtag ctatggcatg 120

<210> 82
 <211> 120
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 82
 cggcccttca cactgtctgg ataataggtg ctaccacccat tactattaat ggttgcgacc 60
 aactccagcc tcttgtctgg agtctggcga acccaagaca tgccatagct actgaaagtg 120

<210> 83
 <211> 118
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 83
 ccagacagtg tgaagggccg attcaccatc tccagagaca atgccaagaa caccctgtac 60
 ctgcaaatga gcagtctgaa gtctgaggac acagccatgt attactgtgc aagagatc 118

<210> 84
 <211> 118
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 84
 cggcgatcca ccgctccgcg tgctctcgcc acctgaggag acggtgaccg tggctccctgg 60
 gccccagtag tcaaatccct cgtcgtaacc atcccgatct cttgcacagt aatacatg 118

<210> 85
 <211> 386
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 85
 gggggatccg gtggcgagg ctgggacatt gagctgaccc aatctccatc aatcatgtct 60
 gcatctccag gggagaaggt caccatgacc tgcagtgccg gctcaagtgt aagttacatg 120

cactgggtacc agcagaagtc aggcacctcc cccaaaagat ggatttatga cacatccaaa 180
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 acaatcagca gcatggaggc tgaagatgct gccacttatt actgccagca gtggagtagt 300
 aaccacacca cggtcggagg gcggaccaag ctggaactga aacgggcccgc cgagcccaaa 360
 tctcctgaca aaactcacac gtggcg 386

<210> 86
 <211> 109
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 86
 gcggggtccg gtggcggagg ctcgacatt gagctgacct aatctccatc aatcatgtct 60
 gcatctccag gggagaaggc caccatgacc tgcagtgccg gctcaagt 109

<210> 87
 <211> 111
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 87
 gcagggaacc cagaagccag ttggatgtg tcataaatcc atcttttggg ggagggtgcct 60
 gacttctgct ggtaccagtg catgtaactt acacttgagc tggcactgca g 111

<210> 88
 <211> 114
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 88
 ctggcttctg gagtccctgc tcgcttcagt ggcagtgggt ctgggacctc ttactctctc 60
 acaatcagca gcatggaggc tgaagatgct gccacttatt actgccagca gtgg 114

<210> 89
 <211> 114
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 89
 cgccacgtgt gagttttgtc aggagatttg ggctcggcgg ccggtttcag ttccagcttg 60
 gtccgccctc cgaacgtggg tgggttacta ctccactgct ggcagtaata agtg 114

<210> 90
 <211> 399
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 90
 gcgggatccg gtggcggagg ctccgacatt gagctgaccc aatctccatc aatcatgtct 60
 gcatctccag gggagaaggc caccatgacc tgcagtgccca gctcaagtgt aagttacatg 120
 cactgggtacc agcagaagtc aggcacctcc cccaaaagat ggattttatga cacatccaaa 180
 ctggcttctg gagtccctgc tcgcttcagt ggcagtgggt ctgggacctc ttactctctc 240
 acaatcagca gcattggagg tgaagatgct gccacttatt actgccagca gtggagtagt 300
 aaccaccca cggtcggagg gcggaccaag ctggaactga aacgggccgc cggtggcgga 360
 ggcagcggag gcggtggtag cggtggcgga actagtgcg 399

<210> 91
 <211> 127
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 91
 cgcactagtt ccgccaccgc taccaccgcc tccgctgcct ccgccaccgc cgccccgttt 60
 cagttccagc ttggtccgcc ctccgaacgt ggggtgggta ctaetccact gctggcagta 120
 ataagtg 127

<210> 92
 <211> 812
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 92
 ttctactagt gtggcggagg cagcggaggc ggtggtagcc aggttcagtt gcagcagtcct 60
 gacgctgagtg tggtagaaacc tggggcttca gtgaagattt cctgcaaggc ttctggctac 120
 accttactctg accatgcaat tcactgggtg aaacagaacc ctgaacaggc cctggaatgg 180
 attggatatt ttttcccg aaatgatgat tttaataca atgagaggtt caaggccaag 240
 gccacactga ctgcagacaa atcctccagc actgcctacg tgcagctcaa cagcctgaca 300
 tctgaggatt ctgcagtgtt ttctgtacc agatccctga atatggccta ctgggggtcaa 360
 ggaacctcag tcacctctc ctcaggtggc ggaggcagcg gaggcggtgg ctccggaggc 420
 ggaggctcgg acattgtgat gtcacagtct ccctctccc tacctgtgtc agttggcgag 480
 aaggttactt tgagctgcaa gtccagtcag agccttttat atagtggtaa tcaaaagaac 540
 tacttggcct ggtaccagca gaaaccaggc cagtctccta aactgctgat ttactgggca 600
 tccgctaggg aatctgggt cctgatcgc ttcacaggca gtggatctgg gacagatttc 660
 actctctcca tcagcagtg gaagactgaa gacctggcag ttattactg tcagcagtat 720
 tatagctatc ccttcaggt cggtgctggg accaagctgg tgctgaaacg ggccgcccag 780
 cccaaatctc ctgacaaaac tcacacgtgc cc 812

<210> 93
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 93
 ttctactagt gtggcggagg cagcggaggc ggtggtagcc aggttcagtt gcagcagtcct 60
 gacg 64

<210> 94
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 94

gggcacgtgt gagttttgtc agg

23

<210> 95

<211> 817

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 95

cttcctgtca gtaactaccg gtgtccactc ccaggttcag ttgcagcagt ctgacgctga 60

gttggtgaaa cctggggcct cagtgaagat ttctctgcaag gcttctggct acaccttcac 120

tgaccatgca attcactggg tgaacacagaa ccctgaacag ggcctggaat ggattggata 180

tttttctccc ggaaatgatg attttaata caatgagagg ttcaagggca aggccacact 240

gactgcagac aaatcctcca gcaactgccta cgtgcagctc aacagcctga catctgagga 300

ttctgcagtg tatttctgta ccagatccct gaatatggcc tactggggtc aaggaaacctc 360

agtcaccgtc tctcagggtg gcggaggcag cggaggcggt ggctccggag gcggaggctc 420

ggacattgtg atgtcacagt ctccatctc cctacctgtg tcagttggcg agaaggttac 480

tttgagctgc aagtcagtc agagcctttt atatagtggt aatcaaaaga actactggc 540

ctgggtaccag cagaaaccag ggcagctctcc taaactgctg atttactggg catccgctag 600

ggaatctggg gtccctgate gcttcacagg cagtggatct gggacagatt tcaactctctc 660

catcagcagt gtgaagactg aagacctggc agtttattac tgtcagcagt attatagcta 720

tccccctcacg ttccgtgctg ggaccaagct ggtgctgaaa cgggccgccg gtggcggagg 780

cagcggaggc ggtggtagcg gtggcggaac tagtaaa 817

<210> 96

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 96
 cttcctgtca gtaactaccg gtgtccactc ccaggttcag 40

<210> 97
 <211> 85
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 97
 tttactagtt ccgccaccgc taccaccgcc tccgtgcct ccgccaccgg cggcccgttt 60
 cagcaccagc ttggtcccag caccg 85

<210> 98
 <211> 806
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 98
 tttactagtg gtggcggagg cagcggaggc ggtggtagcc aggtccaact gcaggagtca 60
 ggaggaggct tagtgcagcc tggagggtcc ctgaaactct cctgtgcagc ctctggattc 120
 actttcagta gctatggcat gtcttgggtt cgccagactc cagacaagag gctggagttg 180
 gtcgcaacca ttaatagtaa tgggtgtagc acctattatc cagacagtgt gaagggccga 240
 ttcaccatct ccagagacaa tgccaagaac acctgtacc tgcaaatgag cagtctgaag 300
 tctgaggaca cagccatgta ttactgtgca agagatcggg atggttacga cgagggattt 360
 gactactggg gccacgggac cagcgtcacc gtctcctcag gtggcggagg cagcggaggc 420
 ggtggatccg gtggcggagg ctcgacatt gagctgaccc aatctccatc aatcatgtct 480
 gcatctccag gggagaaggc caccatgacc tgcagtgcc agetcaagtgt aagttacatg 540
 cactggatcc agcagaagtc aggcacctcc cccaaaagat ggattttatga cacatccaaa 600
 ctggcttctg gactccctgc tcgcttcagt ggcagtgggt ctgggacctc ttactctctc 660
 acaatcagca gcatggaggc tgaagatgct gccacttatt actgccagca gtggagtagt 720
 aacccaccca cgttcggagg gcggaccaag ctggaactga aacggggcgc cgagcccaaa 780
 tctcctgaca aaactcacac gtgccc 806

<210> 99
 <211> 65
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

 <400> 99
 ttctactagtgt gtggcggagg cagcggaggc ggtggtagcc aggtccaact gcaggagtca 60
 ggagg 65

 <210> 100
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

 <400> 100
 acaacggaat tcaagcctgt agcacatggt gtagc 35

 <210> 101
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

 <400> 101
 ggcgggatcc tcacagggca atgatcccaa agtagacct 39

 <210> 102
 <211> 99
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

 <400> 102
 aacaacggaa ttcgaccac ggtccaccc tctctccct ggaaaggaca ccatgagcac 60
 tgaaagcatg atccgggacg tggagctggc cgaggaggc 99

<210> 103
 <211> 99
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 103
 tgccacgac aggaaggaga agaggctgag gaacaagcac cgcctggagc cctggggccc 60
 cctgtcttc ttggggagcg cctcctcggc cagctccac 99

<210> 104
 <211> 99
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 104
 tctcctcct gatcgtagga ggcgccacca cgctcttctg cctgctgcac ttggagtgga 60
 tcggccccca gaggaagag tccccaggg acctctctc 99

<210> 105
 <211> 63
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 105
 ttggctacaa catgtgctac tgcttggccc agagggtga ttagagagag gtcctctggg 60
 aac 63

<210> 106
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 106
 aacaacggaa ttcgacccac 20

<210> 107
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 107
 ttggctacaa catgtgtctac 20

<210> 108
 <211> 717
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (46)..(708)

<400> 108
 gaattcgacc cacggtccca ccctctctccc cctggaaagg acacc atg agc act gaa 57
 Met Ser Thr Glu
 1

agc atg atc cgg gac gtg gag ctg gcc gag gag gcg ctc ccc aag aag 105
 Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala Leu Pro Lys Lys
 5 10 15 20

aca ggg ggg ccc cag ggc tcc agg cgg tgc ttg ttc ctc agc ctc ttc 153
 Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe Leu Ser Leu Phe
 25 30 35

tcc ttc ctg atc gtg gca ggc gcc acc acg ctc ttc tgc ctg ctg cac 201
 Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe Cys Leu Leu His
 40 45 50

ttt gga gtg atc ggc ccc cag agg gaa gag ttc ccc agg gac ctc tct 249
 Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro Arg Asp Leu Ser
 55 60 65

cta atc agc cct ctg gcc cag gca gta gca cat gtt gta gca aac cct 297
 Leu Ile Ser Pro Leu Ala Gln Ala Val Ala His Val Val Ala Asn Pro
 70 75 80

caa gct gag ggg cag ctc cag tgg ctg aac cgc cgg gcc aat gcc ctc 345
 Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
 85 90 95 100

ctg gcc aat ggc gtg gag ctg aga gat aac cag ctg gtg gtg cca tca 393
 Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
 105 110 115

gag ggc ctg tac ctc atc tac tcc cag gtc ctc ttc aag ggc caa ggc 441
 Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
 120 125 130

tgc ccc tcc acc cat gtg ctc ctc acc cac acc atc agc cgc atc gcc 489
 Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
 135 140 145

gtc tcc tac cag acc aag gtc aac ctc ctc tct gcc atc aag agc ccc 537
 Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
 150 155 160

tgc cag agg gag acc cca gag ggg gct gag gcc aag ccc tgg tat gag 585
 Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
 165 170 175 180

ccc atc tat ctg gga ggg gtc ttc cag ctg gag aag ggt gac cga ctc 633
 Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
 185 190 195

agc gct gag atc aat cgg ccc gac tat ctc gac ttt gcc gag tct ggg 681
 Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
 200 205 210

cag gtc tac ttt ggg atc att gcc ctg tgaggatcc 717
 Gln Val Tyr Phe Gly Ile Ile Ala Leu
 215 220

<210> 109

<211> 221

<212> PRT

<213> Homo sapiens

<400> 109

Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
 1 5 10 15

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
 20 25 30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
 35 40 45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Phe Pro
 50 55 60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Ala His Val
 65 70 75 80

Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
 85 90 95

Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
 100 105 110

Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
 115 120 125

Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
 130 135 140

Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
 145 150 155 160

Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
 165 170 175

Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
 180 185 190

Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
 195 200 205

Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
 210 215 220

<210> 110

<211> 383

<212> DNA

<213> *Cricetulus griseus*

<400> 110

gttaactggg gctcttttaa accctgaatt tttctaaatc cccacctcca agagtgttgg 60

ttaaactgat ttttttaatg aatacctttt gaagaataga gcattgtctc atcatgcaaa 120

gctcttcagg gattcagcta gcatgttgaa gaaacataag ggtgttaaat tgtttgtcac 180

aagtgtctgaa taaatattga cgtagtcttc agctattcta tactggaagt agatgatatt 240

ctcatggaa attctgttag gaagtaacct ttctgtctt cttacctgca tagaatccca 300

ggatataaaa cttgtgcttg tcgcccttgc cattgtctct cactgggtgc ctttattgca 360

tctcatatct gccttctctt tcc 383

<210> 111

<211> 564

<212> DNA

<213> *Cricetulus griseus*

<400> 111
 taagaattcc tgtgcccagc tgtatgtgag gctctctgca ggtgtaggga tgtttctgct 60
 tctttcttgc acatgcttca cagctgaagt cctttgggtg tgagattgac attcagatag 120
 actaaagtga ctggacttgt tgggaaacat actgtatgca ttattgccgt tgcctgcagg 180
 tgaaattaac acctcattca ccaatccctg ttcattccaa cttctctacc acatcacttt 240
 aaatagaaat tagacccaat atgactcctt ttttcctaag ctgtttatag agattgtgct 300
 ggagcagtgga gcttttgtgt ttgtttgttt gttttgtaat tttcccatg aaaattcttc 360
 taaactcaaa cctaagaggg aaaaaaaaaa aacagactta tatgtgccac acttgtaaaa 420
 aaaaatcatg aaagatgtat atgatatatt taaacagttt gaattattaag atcacaattt 480
 ctattttaaa aacaatcttg ttttacatat caatcaccca attcccttgc cttcccatcc 540
 tccattccc cccactgac cccc 564

<210> 112
 <211> 120
 <212> DNA
 <213> *Cricetulus griseus*

<400> 112
 atgaatgttc attctttggg tatatgccca agagtagaat tgcataatat tgaggttagac 60
 tgattcccat tttcttgagg agtcgccata ttgatttcca aagtgactgt acaagttaac 120

<210> 113
 <211> 274
 <212> DNA
 <213> *Cricetulus griseus*

<400> 113
 aggcactagg taaatatttt tgaagaaaga atgagtatct cctatttcag aaaaactttt 60
 attgacttaa atttaggata tcagaattag aaaacagtaa aaatttatag gagagttttt 120
 aatgaatgtt attttaagg tccatacaaa tagtaattaa aacttacaca aactatttgt 180
 agtaatgatt cagctcggtg taccctgatg agcattatag acttttaaat tctttttgtg 240
 aattttttta ttagttcaaa ttaggaacaa gctt 274